PCT10

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/030,225

DATE: 08/06/2002
TIME: 12:46:36

Input Set : A:\84335153.app
Output Set: N:\CRF3\08062002\J030225.raw

ENTERED

<110> APPLICANT: OTA, TOSHIO
ISOGAI, TAKAO
NISHIKAWA, TETSUO
HIO, YURI
KENJI, YOSHIDA
MASUHO, YASUHIKO
<120> TITLE OF INVENTION: GROWTH AND DIFFERENTIATION FACTOR
<130> FILE REFERENCE: 084335/0153
<140> CURRENT APPLICATION NUMBER: 10/030,225
<141> CURRENT FILING DATE: 2002-01-08
<150> PRIOR APPLICATION NUMBER: JP 11/194179
<151> PRIOR FILING DATE: 1999-07-08
<150> PRIOR APPLICATION NUMBER: 60/159,586
<151> PRIOR FILING DATE: 1999-10-18
<160> NUMBER OF SEQ ID NOS: 14
<170> SOFTWARE: PatentIn Ver. 2.1
<210> SEQ ID NO: 1
<211> LENGTH: 2981
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (58)..(1770)
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Met Arg Ala Leu Arg Asp Arg Ala Gly Leu Leu Leu Cys Val Leu Leu
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ctg gcg gcg ctg ctg gag gcg gcg cta ggg ctc ccc gtg aag aag ccg    153
Leu Ala Ala Leu Leu Glu Ala Ala Leu Gly Leu Pro Val Lys Lys Pro
            20                  25                  30
cgg ctc cgc gga cca cgg cct ggg agc ctc acg agg ctc gca gag gtc    201
Arg Leu Arg Gly Pro Arg Pro Gly Ser Leu Thr Arg Leu Ala Glu Val
        35                  40                  45
tca gcc tcc cca gat cct agg cct ctg aag gaa gag gag gag gca cca    249
Ser Ala Ser Pro Asp Pro Arg Pro Leu Lys Glu Glu Glu Glu Ala Pro
    50                  55                  60
ctg ctc ccc aga acc cac ctg cag gca gag cca cac caa cat gga tgc    297
Leu Leu Pro Arg Thr His Leu Gln Ala Glu Pro His Gln His Gly Cys
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tgg act gtc act gag cca gca gcc atg acc cca ggc aac acc acc cct    345
Trp Thr Val Thr Glu Pro Ala Ala Met Thr Pro Gly Asn Thr Thr Pro
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67 ccg gga ttg gcc agc aca acc ttg agt acc cct aac cct gat acc cag   441
68 Pro Gly Leu Ala Ser Thr Thr Leu Ser Thr Pro Asn Pro Asp Thr Gln
69         115                 120                 125
71 gct tca gcc tcc cca gat cct agg cct ctg agg gaa gag gag gag gca   489
72 Ala Ser Ala Ser Pro Asp Pro Arg Pro Leu Arg Glu Glu Glu Glu Ala
73     130                 135                 140
75 cga ctg ctc ccc aga acc cac ctg cag gca gag cta cac caa cat gga   537
76 Arg Leu Leu Pro Arg Thr His Leu Gln Ala Glu Leu His Gln His Gly
77 145                 150                 155                 160
79 tgt tgg act gtc act gag cca gca gcc ctg acc cca ggg aat gcc acg   585
80 Cys Trp Thr Val Thr Glu Pro Ala Ala Leu Thr Pro Gly Asn Ala Thr
81                 165                 170                 175
83 cct ccc agg acc cag gag gtt act ccc ttg ctg ctg gag ctg cag aag   633
84 Pro Pro Arg Thr Gln Glu Val Thr Pro Leu Leu Leu Glu Leu Gln Lys
85             180                 185                 190
87 ctg cca gaa ttg gtc cac gca acc ttg agt acc cct aac cct gat aac   681
88 Leu Pro Glu Leu Val His Ala Thr Leu Ser Thr Pro Asn Pro Asp Asn
89         195                 200                 205
91 cag gtg acc atc aag gtg gtg gag gac ccc cag gcc gag gtg tcg ata   729
92 Gln Val Thr Ile Lys Val Val Glu Asp Pro Gln Ala Glu Val Ser Ile
93     210                 215                 220
95 gac ctg ttg gct gag ccc agc aat ccc ccg ccc cag gat acc ctt agc   777
96 Asp Leu Leu Ala Glu Pro Ser Asn Pro Pro Pro Gln Asp Thr Leu Ser
97 225                 230                 235                 240
99 tgg ctg ccc gcc ctc tgg ccc ttc ctc tgg gga gac tac aaa gga gag   825
100 Trp Leu Pro Ala Leu Trp Pro Phe Leu Trp Gly Asp Tyr Lys Gly Glu
101                 245                 250                 255
103 gaa aaa gac agg gcc cca ggg gag aag ggg gag gaa aag gag gaa gac   873
104 Glu Lys Asp Arg Ala Pro Gly Glu Lys Gly Glu Glu Lys Glu Glu Asp
105             260                 265                 270
107 gag gac tat cct tca gag gat atc gag ggt gag gat caa gag gac aaa   921
108 Glu Asp Tyr Pro Ser Glu Asp Ile Glu Gly Glu Asp Gln Glu Asp Lys
109         275                 280                 285
111 gag gaa gat gag gaa gag cag gcg ctc tgg ttc aat gga act aca gac   969
112 Glu Glu Asp Glu Glu Glu Gln Ala Leu Trp Phe Asn Gly Thr Thr Asp
113     290                 295                 300
115 aac tgg gac cag ggc tgg ctg gcc ccc ggg gat tgg gtc ttc aag gat   1017
116 Asn Trp Asp Gln Gly Trp Leu Ala Pro Gly Asp Trp Val Phe Lys Asp
117 305                 310                 315                 320
119 tct gtc agc tac gac tat gag cct cag aag gag tgg agt ccc tgg tct   1065
120 Ser Val Ser Tyr Asp Tyr Glu Pro Gln Lys Glu Trp Ser Pro Trp Ser
121                 325                 330                 335
123 ccc tgc agt ggg aac tgc agc act ggc aag cag cag agg act cgg ccc   1113
124 Pro Cys Ser Gly Asn Cys Ser Thr Gly Lys Gln Gln Arg Thr Arg Pro
125             340                 345                 350
127 tgt ggc tat ggc tgc act gcc acc gag acc cgt acc tgt gac ctg ccc   1161
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131 tcc tgt cct ggc act gag gac aag gac acc ttg ggc ctc ccc agt gag   1209
132 Ser Cys Pro Gly Thr Glu Asp Lys Asp Thr Leu Gly Leu Pro Ser Glu
133     370                 375                 380
135 gag tgg aag ctc ctg gcc cgc aat gct acg gac atg cat gat caa gat   1257
136 Glu Trp Lys Leu Leu Ala Arg Asn Ala Thr Asp Met His Asp Gln Asp
137 385                 390                 395                 400
139 gtg gac agc tgt gag aag tgg ctg aac tgc aag agc gac ttc cta atc   1305
140 Val Asp Ser Cys Glu Lys Trp Leu Asn Cys Lys Ser Asp Phe Leu Ile
141                 405                 410                 415
143 aag tat ctg agc cag atg ctg cgg gac ctg ccc agc tgc ccg tgt gcc   1353
144 Lys Tyr Leu Ser Gln Met Leu Arg Asp Leu Pro Ser Cys Pro Cys Ala
145             420                 425                 430
147 tac cca ctg gag gcc atg gac agc cct gtg agc cta cag gac gag cac   1401
148 Tyr Pro Leu Glu Ala Met Asp Ser Pro Val Ser Leu Gln Asp Glu His
149         435                 440                 445
151 cag ggc cgc agc ttc cgg tgg agg gat gcc agt ggc cct cgc gag cgc   1449
152 Gln Gly Arg Ser Phe Arg Trp Arg Asp Ala Ser Gly Pro Arg Glu Arg
153     450                 455                 460
155 ctg gac atc tac cag ccc acg gcg cgc ttc tgc ctg cgt tcc atg ctg   1497
156 Leu Asp Ile Tyr Gln Pro Thr Ala Arg Phe Cys Leu Arg Ser Met Leu
157 465                 470                 475                 480
159 tct ggg gag agc agc aca ctg gcc gcc cag cac tgc tgc tat gac gag   1545
160 Ser Gly Glu Ser Ser Thr Leu Ala Ala Gln His Cys Cys Tyr Asp Glu
161                 485                 490                 495
163 gac agc cgg ctg ctg acc cgt ggc aag ggc gcc ggc atg ccc aac ctc   1593
164 Asp Ser Arg Leu Leu Thr Arg Gly Lys Gly Ala Gly Met Pro Asn Leu
165             500                 505                 510
167 atc agc acc gac ttc tca cct aag ctg cac ttc aag ttc gac acg acg   1641
168 Ile Ser Thr Asp Phe Ser Pro Lys Leu His Phe Lys Phe Asp Thr Thr
169         515                 520                 525
171 ccc tgg atc ctg tgc aag ggg gac tgg agc cgc ctc cac gct gtg ctc   1689
172 Pro Trp Ile Leu Cys Lys Gly Asp Trp Ser Arg Leu His Ala Val Leu
173     530                 535                 540
175 cct ccc aac aac ggc cga gcc tgc acc gac aac ccc ctg gag gag gag   1737
176 Pro Pro Asn Asn Gly Arg Ala Cys Thr Asp Asn Pro Leu Glu Glu Glu
177 545                 550                 555                 560
179 tac cta gca cag ttg cag gag gcc aag gag tac tagtgacggg gttgctgaac 1790
180 Tyr Leu Ala Gln Leu Gln Glu Ala Lys Glu Tyr
181                 565                 570
183 agacactgca gggagagggc aggcggctgc tgctgttgca cgggagaact ttcctggtag 1850
185 ggccctcacc cgcccctgcc cagacagggt gaggaaaggg ctcccccagt gaggttggtc 1910
187 cgaggctgtg tgccctctgc cagcgacccc gaagcagata tctcagtggg gttagtgaga 1970
189 aggttgaagg gtatgtaggg cccagggtgg gtgtccctgg gagccctgga aatgtgcata 2030
191 tgtgcatgtg tctgccgggg cctccctctg ctgcctgctg ggaccctggc cactcatttt 2090
193 tctcctcctt gggagctggg ctcttctgcc ctggctctgc acataagtgt tagccagcag 2150
195 ctccagaaaa atcccgattc ccgggatctg ccacgagtca ctcctactcc accctgatgg 2210
197 ccagcagagg aagggccact cttctcatgg gcacagccat cctttgccgg gggggcatcc 2270
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205 gaatgggttg cccaattctg gtcccttccc tttgctcagc cccctctgtt ctgctgattg 2510
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215 ctcagagttg ggaagagatg cacataatcg ctctcccggc acacctcatg cctcttccct 2810
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225 <211> LENGTH: 571
226 <212> TYPE: PRT
227 <213> ORGANISM: Homo sapiens
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234              20                  25                  30
236 Arg Leu Arg Gly Pro Arg Pro Gly Ser Leu Thr Arg Leu Ala Glu Val
237          35                  40                  45
239 Ser Ala Ser Pro Asp Pro Arg Pro Leu Lys Glu Glu Glu Glu Ala Pro
240      50                  55                  60
242 Leu Leu Pro Arg Thr His Leu Gln Ala Glu Pro His Gln His Gly Cys
243  65                  70                  75                  80
245 Trp Thr Val Thr Glu Pro Ala Ala Met Thr Pro Gly Asn Thr Thr Pro
246                  85                  90                  95
248 Pro Arg Thr Pro Glu Val Thr Pro Leu Arg Leu Glu Leu Gln Lys Leu
249             100                 105                 110
251 Pro Gly Leu Ala Ser Thr Thr Leu Ser Thr Pro Asn Pro Asp Thr Gln
252         115                 120                 125
254 Ala Ser Ala Ser Pro Asp Pro Arg Pro Leu Arg Glu Glu Glu Glu Ala
255     130                 135                 140
257 Arg Leu Leu Pro Arg Thr His Leu Gln Ala Glu Leu His Gln His Gly
258 145                 150                 155                 160
260 Cys Trp Thr Val Thr Glu Pro Ala Ala Leu Thr Pro Gly Asn Ala Thr
261                 165                 170                 175
263 Pro Pro Arg Thr Gln Glu Val Thr Pro Leu Leu Leu Glu Leu Gln Lys
264             180                 185                 190
266 Leu Pro Glu Leu Val His Ala Thr Leu Ser Thr Pro Asn Pro Asp Asn
267         195                 200                 205
269 Gln Val Thr Ile Lys Val Val Glu Asp Pro Gln Ala Glu Val Ser Ile
270     210                 215                 220
272 Asp Leu Leu Ala Glu Pro Ser Asn Pro Pro Pro Gln Asp Thr Leu Ser
273 225                 230                 235                 240
275 Trp Leu Pro Ala Leu Trp Pro Phe Leu Trp Gly Asp Tyr Lys Gly Glu
276                 245                 250                 255
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279             260                 265                 270
281 Glu Asp Tyr Pro Ser Glu Asp Ile Glu Gly Glu Asp Gln Glu Asp Lys
282         275                 280                 285
284 Glu Glu Asp Glu Glu Glu Gln Ala Leu Trp Phe Asn Gly Thr Thr Asp
285     290                 295                 300
287 Asn Trp Asp Gln Gly Trp Leu Ala Pro Gly Asp Trp Val Phe Lys Asp
288 305                 310                 315                 320
290 Ser Val Ser Tyr Asp Tyr Glu Pro Gln Lys Glu Trp Ser Pro Trp Ser
291                 325                 330                 335
293 Pro Cys Ser Gly Asn Cys Ser Thr Gly Lys Gln Gln Arg Thr Arg Pro
294             340                 345                 350
296 Cys Gly Tyr Gly Cys Thr Ala Thr Glu Thr Arg Thr Cys Asp Leu Pro
297         355                 360                 365
299 Ser Cys Pro Gly Thr Glu Asp Lys Asp Thr Leu Gly Leu Pro Ser Glu
300     370                 375                 380
302 Glu Trp Lys Leu Leu Ala Arg Asn Ala Thr Asp Met His Asp Gln Asp
303 385                 390                 395                 400
305 Val Asp Ser Cys Glu Lys Trp Leu Asn Cys Lys Ser Asp Phe Leu Ile
306                 405                 410                 415
308 Lys Tyr Leu Ser Gln Met Leu Arg Asp Leu Pro Ser Cys Pro Cys Ala
309             420                 425                 430
311 Tyr Pro Leu Glu Ala Met Asp Ser Pro Val Ser Leu Gln Asp Glu His
312         435                 440                 445
314 Gln Gly Arg Ser Phe Arg Trp Arg Asp Ala Ser Gly Pro Arg Glu Arg
315     450                 455                 460
317 Leu Asp Ile Tyr Gln Pro Thr Ala Arg Phe Cys Leu Arg Ser Met Leu
318 465                 470                 475                 480
320 Ser Gly Glu Ser Ser Thr Leu Ala Ala Gln His Cys Cys Tyr Asp Glu
321                 485                 490                 495
323 Asp Ser Arg Leu Leu Thr Arg Gly Lys Gly Ala Gly Met Pro Asn Leu
324             500                 505                 510
326 Ile Ser Thr Asp Phe Ser Pro Lys Leu His Phe Lys Phe Asp Thr Thr
327         515                 520                 525
329 Pro Trp Ile Leu Cys Lys Gly Asp Trp Ser Arg Leu His Ala Val Leu
330     530                 535                 540
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336                 565                 570
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348 <400> SEQUENCE: 3
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VERIFICATION SUMMARY
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